



SEQUENCE LISTING

<110> Brooks, Alan R.  
Deng, Gary G.  
Rubanyi, Gabor M.  
Schering Aktiengesellschaft

<120> Estrogen-Regulated Unconventional Myosin-Related  
Protein: Compositions and Methods of Use

<130> 015303-000310US

<140> US 09/803,126

<141> 2001-03-09

<150> US 60/188,488

<151> 2000-03-10

<160> 35

<170> PatentIn Ver. 2.1

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<213> Homo sapiens

<220>

<223> Partial DNA sequence for human myosin related  
 protein variant 1 (hMRP1)

<400> 5

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 ggtggctgcc tgagggagac ctccgaggag gctgaagaca ggccctatca gcccaagagc 180  
 ttccagcaga aacggaacta tttccagagg atggggcagc cacagatcac agtgaggacg 240  
 atgaagcccc cggccaaggt ccacatcccc cagggggaag cgcaggagga ggaggaggag 300  
 gaggaggagg aggaggagca ggaggagcaa gaagtggaaa caagagcagc gccgtcccct 360  
 cctcctcccc ccatcgtgaa gaagccattg aagcaagggt gggccaaagc tccaaaagag 420  
 gctgaggctg agccagccaa ggagacagcg gccaaaggcc atggccaagg gccagcccaa 480  
 ggcaggggga ctgtggtgcg cagtcagact ccaagcccaa gcggccacaa cccagcaggg 540  
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 agccatccag gcctcccaaa gctttcctga ggaaaatcga cccaaggac gaggtctg 660  
 ccaagctggg tatcaacggt gcccaactcg ccccgccgat gctgtccccc agcccaggaa 720  
 agggccccc gccagctgtg gctcctcgac ccaaggcccc gctacagctt gggccctcta 780  
 gctccatcaa ggaaaagcag gggccccttc tggacctgtt tggccagaag ctgcctattg 840  
 cccacacacc cccacctcca ccagcgccac cactgcctct gcccgaggac ccagggaccc 900  
 ttccagcaga gcgtcgttgc ttgacacagc ccgtggagga ccaggggggc tccaccagc 960  
 tactcgcgcc ctctggcagc gtgtgcttct cctacaccgg cacgccctgg aagttgttcc 1020



<210> 6  
 <211> 786  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Partial amino acid sequence of human myosin  
 related protein variant 2 (hMRP2)

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 Arg Pro Pro Lys Ala Phe Leu Arg Lys Ile Asp Pro Lys Asp Glu Ala  
           20                  25                  30  
 Leu Ala Lys Leu Gly Ile Asn Gly Ala His Ser Ser Pro Pro Met Leu  
       35                  40                  45  
 Ser Pro Ser Pro Gly Lys Gly Pro Pro Pro Ala Val Ala Pro Arg Pro  
       50                  55                  60  
 Lys Ala Pro Leu Gln Leu Gly Pro Ser Ser Ser Ile Lys Glu Lys Gln  
       65                  70                  75                  80  
 Gly Pro Leu Leu Asp Leu Phe Gly Gln Lys Leu Pro Ile Ala His Thr  
           85                  90                  95  
 Pro Pro Pro Pro Pro Ala Pro Pro Leu Pro Leu Pro Glu Asp Pro Gly  
       100                  105                  110  
 Thr Leu Ser Ala Glu Arg Arg Cys Leu Thr Gln Pro Val Glu Asp Gln  
       115                  120                  125  
 Gly Val Ser Thr Gln Leu Leu Ala Pro Ser Gly Ser Val Cys Phe Ser  
       130                  135                  140  
 Tyr Thr Gly Thr Pro Trp Lys Leu Phe Leu Arg Lys Glu Val Phe Tyr  
       145                  150                  155                  160  
 Pro Arg Glu Asn Phe Ser His Pro Tyr Tyr Leu Arg Leu Leu Cys Glu  
           165                  170                  175  
 Gln Ile Leu Arg Asp Thr Phe Ser Glu Ser Cys Ile Arg Ile Ser Gln  
       180                  185                  190  
 Asn Glu Arg Arg Lys Met Lys Asp Leu Leu Gly Gly Leu Glu Val Asp  
       195                  200                  205  
 Leu Asp Ser Leu Thr Thr Thr Glu Asp Ser Val Lys Lys Arg Ile Val  
       210                  215                  220  
 Val Ala Ala Arg Asp Asn Trp Ala Asn Tyr Phe Ser Arg Phe Phe Pro  
       225                  230                  235                  240  
 Val Ser Gly Glu Ser Gly Ser Asp Val Gln Leu Leu Ala Val Ser His  
           245                  250                  255  
 Arg Gly Leu Arg Leu Leu Lys Val Thr Gln Gly Pro Gly Leu Arg Pro  
       260                  265                  270

Asp Gln Leu Lys Ile Leu Cys Ser Tyr Ser Phe Ala Glu Val Leu Gly  
 275 280 285  
 Val Glu Cys Arg Gly Gly Ser Thr Leu Glu Leu Ser Leu Lys Ser Glu  
 290 295 300  
 Gln Leu Val Leu His Thr Ala Arg Ala Arg Ala Ile Glu Ala Leu Val  
 305 310 315 320  
 Glu Leu Phe Leu Asn Glu Leu Lys Lys Asp Ser Gly Tyr Val Ile Ala  
 325 330 335  
 Leu Arg Ser Tyr Ile Thr Asp Asn Cys Ser Leu Leu Ser Phe His Arg  
 340 345 350  
 Gly Asp Leu Ile Lys Leu Leu Pro Val Ala Thr Leu Glu Pro Gly Trp  
 355 360 365  
 Gln Phe Gly Ser Ala Gly Gly Arg Ser Gly Leu Phe Pro Ala Asp Ile  
 370 375 380  
 Val Gln Pro Ala Ala Ala Pro Asp Phe Ser Phe Ser Lys Glu Gln Arg  
 385 390 395 400  
 Ser Gly Trp His Lys Gly Gln Leu Ser Asn Gly Glu Pro Gly Leu Ala  
 405 410 415  
 Arg Trp Asp Arg Ala Ser Glu Arg Pro Ala His Pro Trp Ser Gln Ala  
 420 425 430  
 His Ser Asp Asp Ser Glu Ala Thr Ser Leu Ser Ser Val Ala Tyr Ala  
 435 440 445  
 Phe Leu Pro Asp Ser His Ser Tyr Thr Met Gln Glu Phe Ala Arg Arg  
 450 455 460  
 Tyr Phe Arg Arg Ser Gln Ala Leu Leu Gly Gln Thr Asp Gly Gly Ala  
 465 470 475 480  
 Ala Gly Lys Asp Thr Asp Ser Leu Val Gln Tyr Thr Lys Ala Pro Ile  
 485 490 495  
 Gln Glu Ser Leu Leu Ser Leu Ser Asp Asp Val Ser Lys Leu Ala Val  
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 Ala Ser Phe Leu Ala Leu Met Arg Phe Met Gly Asp Gln Ser Lys Pro  
 515 520 525  
 Arg Gly Lys Asp Glu Met Asp Leu Leu Tyr Glu Leu Leu Lys Leu Cys  
 530 535 540  
 Gln Gln Glu Lys Leu Arg Asp Glu Ile Tyr Cys Gln Val Ile Lys Gln  
 545 550 555 560  
 Val Thr Gly His Pro Arg Pro Glu His Cys Thr Arg Gly Trp Ser Phe  
 565 570 575  
 Leu Ser Leu Leu Thr Gly Phe Phe Pro Pro Ser Thr Arg Leu Met Pro  
 580 585 590  
 Tyr Leu Thr Lys Phe Leu Gln Asp Ser Gly Pro Ser Gln Glu Leu Ala

595	600	605
Arg Ser Ser Gln Glu His Leu Gln Arg Thr Val Lys Tyr Gly Gly Arg		
610	615	620
Arg Arg Met Pro Pro Pro Gly Glu Met Lys Ala Phe Leu Lys Gly Gln		
625	630	635
Ala Ile Arg Leu Leu Leu Ile His Leu Pro Gly Gly Val Asp Tyr Arg		
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Thr Asn Ile Gln Thr Phe Thr Val Ala Ala Glu Val Gln Glu Glu Leu		
	660	665
Cys Arg Gln Met Gly Ile Thr Glu Pro Gln Glu Val Gln Glu Phe Ala		
	675	680
Leu Phe Leu Ile Lys Glu Lys Ser Gln Leu Val Arg Pro Leu Gln Pro		
	690	700
Ala Glu Tyr Leu Asn Ser Val Val Val Asp Gln Asp Val Ser Leu His		
705	710	715
Ser Gly Gly Ser Thr Gly Arg Pro His Cys Thr Ser Ile Thr Pro Pro		
	725	730
Thr Ser Ala Pro Thr Thr Ala Arg Cys Cys Gly Thr Thr Phe Arg Gly		
	740	745
Ser Cys Gln Ser Ala Pro Arg Gln Thr Arg Ser Ser Pro Gly Trp Pro		
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Pro Cys Ser Thr Ser Ala Arg Pro Thr Gly Ile Pro Pro Gln Gly Arg		
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Thr Cys		780
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<210> 7

<211> 3780

<212> DNA

<213> Homo sapiens

<220>

<223> Partial DNA sequence for human myosin related  
protein variant 2 (hMRP2)

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ttccagcaga	aacggaacta	tttccagagg	atggggcagc	cacagatcac	agtgaggacg	240
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gaggaggagg	aggaggagca	ggaggagcaa	gaagtggaaa	caagagcagc	gccgtccctc	360
cctcctcccc	ccatcgtgaa	gaagccattg	aagcaagggtg	gggccaagc	tccaaaagag	420
gctgaggctg	agccagccaa	ggagacagcg	gccaaaggcc	atggccaagg	gccagcccaa	480
ggcaggggga	ctgtggtgcg	cagtcagact	ccaagcccaa	gcggccacaa	cccagcaggg	540
aaattggcaa	catcatccgc	atgtaccaga	gccgcccggg	ccccgtgcct	gtgcccgtgc	600
agccatccag	gcctcccaaa	gctttcctga	ggaaaatcga	cccccaaggac	gaggctctgg	660
ccaagctggg	tatcaacggt	gcccactcgt	ccccgcggat	gctgtccccc	agcccaggaa	720

agggccccc	gccagctgtg	gctcctcgac	ccaaggcccc	gctacagctt	gggccctcta	780
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tactcgcgcc	ctctggcagc	gtgtgcttct	cctacaccgg	cacgccctgg	aaagttgttc	1020
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gtactgccgc	attgccctga	agagcctgca	gcggctccac	ctgctaagcc	ctctggagga	3240
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gatgcccacc	cgaccccagg	ctccgcccag	gccccacatt	agcacaaagcc	caggcatggg	3720
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<211> 21  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Signature  
sequence 1 conserved between mouse and human MRP  
genes, consensus peptides

<400> 8

Pro Trp Lys Leu Phe Leu Arg Lys Glu Val Phe Tyr Pro Arg Glu Asn  
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Phe Ser His Pro Tyr  
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<210> 9  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Signature  
sequence 2 conserved between mouse and human MRP  
genes, consensus peptides

<400> 9

Lys Lys Arg Ile Val Val Ala Ala Arg Asp Asn Trp Ala Asn Tyr Phe  
1 5 10 15

Ser Arg

<210> 10  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Signature  
sequence 3 conserved between mouse and human MRP  
genes, consensus peptides

<400> 10

Lys Asp Ser Gly Tyr Val Ile Ala Leu Arg Ser Tyr Ile Thr Asp  
1 5 10 15



<210> 11  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Signature  
 sequence 4 conserved between mouse and human MRP  
 genes, consensus peptides

<400> 11

Leu Glu Pro Gly Trp Gln Phe Gly Ser Ala Gly Gly Arg Ser Gly Leu  
 1 5 10 15

Phe Pro

<210> 12  
 <211> 407  
 <212> PRT  
 <213> Mus sp.

<220>

<223> partial amino acid sequence for mouse myosin  
 related protein (mMRP)

<400> 12

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Arg Pro Ile Lys Thr Phe Gln Lys Lys Asn Asp Pro Lys Asp Glu Ala  
 20 25 30

Leu Ala Lys Leu Gly Ile Asn Gly Val His Leu Pro Leu Ser Thr Ser  
 35 40 45

Pro Asn Gln Gly Lys Ser Ser Pro Pro Ala Val Val Pro Arg Pro Lys  
 50 55 60

Ala Arg Pro Arg Leu Glu Pro Ser Leu Ser Ile Gln Glu Lys Gln Gly  
 65 70 75 80

Pro Leu Arg Asp Leu Phe Gly Pro Cys Ser Pro Asn Pro Pro Thr Ala  
 85 90 95

Pro Ala Pro Pro Pro Pro Pro Ala Leu Pro Pro Pro Leu Ser Gly Glu  
 100 105 110

Pro Lys Thr Pro Ser Val Glu Ser His Ala Leu Thr Glu Pro Met Glu  
 115 120 125

Asp Lys Asn Ile Ser Thr Lys Leu Leu Val Pro Ser Gly Ser Val Cys  
 130 135 140

Phe Ser Tyr Ala Asn Ala Pro Trp Lys Leu Phe Leu Arg Lys Glu Val  
 145 150 155 160

Phe Tyr Pro Arg Glu Asn Phe Ser His Pro Tyr Cys Leu Ser Leu Leu  
 165 170 175

Cys Gln Gln Ile Leu Arg Asp Thr Phe Thr Glu Ser Cys Thr Arg Ile  
 180 185 190  
 Ser Gln Asp Glu Arg His Lys Met Lys Gly Leu Leu Gly Asp Leu Glu  
 195 200 205  
 Val Ser Leu Glu Thr Leu Asp Ile Val Glu Asp Ser Ile Lys Lys Arg  
 210 215 220  
 Ile Val Val Ala Ala Arg Asp Asn Trp Ala Asn Tyr Phe Ser Arg Ile  
 225 230 235 240  
 Phe Pro Val Ser Gly Glu Ser Gly Ser Asp Val Gln Leu Leu Gly Val  
 245 250 255  
 Ser His Arg Gly Leu Arg Leu Leu Lys Val Thr Gln Ser Pro Ser Phe  
 260 265 270  
 His Leu Asp Gln Leu Lys Thr Leu Cys Ser Tyr Ser Tyr Ala Glu Val  
 275 280 285  
 Leu Thr Val Gln Cys Arg Gly Arg Ser Thr Leu Glu Leu Ser Leu Lys  
 290 295 300  
 Asn Glu Gln Leu Ile Leu His Thr Ala Trp Ala Arg Ala Ile Lys Ala  
 305 310 315 320  
 Met Val Asp Leu Phe Leu Ser Glu Leu Arg Lys Asp Ser Gly Tyr Val  
 325 330 335  
 Ile Ala Leu Arg Ser Tyr Ile Thr Asp Asp Asn Ser Leu Leu Ser Phe  
 340 345 350  
 His Arg Gly Asp Leu Ile Arg Leu Leu Pro Val Thr Ala Leu Glu Pro  
 355 360 365  
 Gly Trp Gln Phe Gly Ser Ala Gly Gly Arg Ser Gly Leu Phe Pro Asp  
 370 375 380  
 Asp Val Val Gln Pro Ala Ala Ala Pro Asp Leu Ser Phe Ser Leu Gly  
 385 390 395 400  
 Lys Arg Asn Ser Trp Gln Arg  
 405

<210> 13  
 <211> 405  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Partial amino acid sequence for human myosin  
 related protein variant 1 (hMRP1)

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 1 5 10 15  
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 20 25 30

Leu Ala Lys Leu Gly Ile Asn Gly Ala His Ser Ser Pro Pro Met Leu  
           35                                  40                                  45  
 Ser Pro Ser Pro Gly Lys Gly Pro Pro Pro Ala Val Ala Pro Arg Pro  
           50                                  55                                  60  
 Lys Ala Pro Leu Gln Leu Gly Pro Ser Ser Ser Ile Lys Glu Lys Gln  
           65                                  70                                  75                                  80  
 Gly Pro Leu Leu Asp Leu Phe Gly Gln Lys Leu Pro Ile Ala His Thr  
                                   85                                  90                                  95  
 Pro Pro Pro Pro Pro Ala Pro Pro Leu Pro Leu Pro Glu Asp Pro Gly  
                                   100                                  105                                  110  
 Thr Leu Ser Ala Glu Arg Arg Cys Leu Thr Gln Pro Val Glu Asp Gln  
                                   115                                  120                                  125  
 Gly Val Ser Thr Gln Leu Leu Ala Pro Ser Gly Ser Val Cys Phe Ser  
                                   130                                  135                                  140  
 Tyr Thr Gly Thr Pro Trp Lys Leu Phe Leu Arg Lys Glu Val Phe Tyr  
                                   145                                  150                                  155                                  160  
 Pro Arg Glu Asn Phe Ser His Pro Tyr Tyr Leu Arg Leu Leu Cys Glu  
                                   165                                  170                                  175  
 Gln Ile Leu Arg Asp Thr Phe Ser Glu Ser Cys Ile Arg Ile Ser Gln  
                                   180                                  185                                  190  
 Asn Glu Arg Arg Lys Met Lys Asp Leu Leu Gly Gly Leu Glu Val Asp  
                                   195                                  200                                  205  
 Leu Asp Ser Leu Thr Thr Thr Glu Asp Ser Val Lys Lys Arg Ile Val  
                                   210                                  215                                  220  
 Val Ala Ala Arg Asp Asn Trp Ala Asn Tyr Phe Ser Arg Phe Phe Pro  
                                   225                                  230                                  235                                  240  
 Val Ser Gly Glu Ser Gly Ser Asp Val Gln Leu Leu Ala Val Ser His  
                                   245                                  250                                  255  
 Arg Gly Leu Arg Leu Leu Lys Val Thr Gln Gly Pro Gly Leu Arg Pro  
                                   260                                  265                                  270  
 Asp Gln Leu Lys Ile Leu Cys Ser Tyr Ser Phe Ala Glu Val Leu Gly  
                                   275                                  280                                  285  
 Val Glu Cys Arg Gly Gly Ser Thr Leu Glu Leu Ser Leu Lys Ser Glu  
                                   290                                  295                                  300  
 Gln Leu Val Leu His Thr Ala Arg Ala Arg Ala Ile Glu Ala Leu Val  
                                   305                                  310                                  315                                  320  
 Glu Leu Phe Leu Asn Glu Leu Lys Lys Asp Ser Gly Tyr Val Ile Ala  
                                   325                                  330                                  335  
 Leu Arg Ser Tyr Ile Thr Asp Asn Cys Ser Leu Leu Ser Phe His Arg  
                                   340                                  345                                  350

Gly Asp Leu Ile Lys Leu Leu Pro Val Ala Thr Leu Glu Pro Gly Trp  
 355 360 365

Gln Phe Gly Ser Ala Gly Gly Arg Ser Gly Leu Phe Pro Ala Asp Ile  
 370 375 380

Val Gln Pro Ala Ala Ala Pro Asp Phe Ser Phe Ser Lys Glu Gln Arg  
 385 390 395 400

Ser Gly Trp His Lys  
 405

<210> 14  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Consensus  
 Peptide

<400> 14  
 Met Tyr Gln Ser Arg Pro Gly Pro Val  
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<210> 15  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Consensus  
 Peptide

<400> 15  
 Val Pro Val Gln  
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<210> 16  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Consensus  
 Peptide

<400> 16  
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<210> 17
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
      Peptide

<400> 17
Pro Pro Ala Val
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<210> 18
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
      Peptide

<400> 18
Pro Arg Pro Lys Ala
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<210> 19
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
      Peptide

<400> 19
Glu Lys Gln Gly Pro Leu
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<210> 20
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
      Peptide

<400> 20
Asp Leu Phe Gly
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<210> 21  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus  
Peptide

<400> 21  
Pro Pro Pro Pro Pro Ala  
1 5

<210> 22  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus  
Peptide

<400> 22  
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1 5

<210> 23  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus  
Peptide

<400> 23  
Gln Ile Leu Arg Asp Thr Phe  
1 5

<210> 24  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus  
Peptide

<400> 24  
Arg Ile Ser Gln  
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<210> 25  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Consensus  
       Peptide  
  
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   1                  5                  10

<210> 26  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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       Peptide

<400> 26  
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<210> 27  
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<220>  
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<210> 28  
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Peptide

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Peptide

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Peptide

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Peptide

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Peptide

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<210> 34  
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Peptide

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<210> 35  
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Peptide

<400> 35  
Val Gln Pro Ala Ala Ala Pro Asp  
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